

## **Exhibit A**

### **Clean Version of The Pending Claims in U.S. Patent Application Ser. No. 09/714,882**

1.(Amended) An isolated nucleic acid molecule comprising the nucleotide sequence shown in SEQ ID NO:1.

2.(Amended) An isolated nucleic acid molecule comprising a nucleotide sequence that encodes the amino acid sequence shown in SEQ ID NO:2.

3. An isolated nucleic acid molecule comprising a nucleotide sequence that encodes the amino acid sequence shown in SEQ ID NO:4.

4. An isolated nucleic acid molecule comprising a nucleotide sequence that encodes the amino acid sequence shown in SEQ ID NO:6.

5 An isolated nucleic acid molecule comprising a nucleotide sequence that encodes the amino acid sequence shown in SEQ ID NO:8.

6. An isolated nucleic acid molecule comprising a nucleotide sequence that encodes the amino acid sequence shown in SEQ ID NO:10.

7.(New) An expression vector comprising a nucleic acid sequence of Claim 2.

8.(New) A cell comprising the expression vector of Claim 7.

## Exhibit B

### **Marked-up Version of The Pending Claims in U.S. Patent Application Ser. No. 09/714,882**

1. An isolated nucleic acid molecule comprising [at least 24 contiguous bases of] the nucleotide sequence [first disclosed in the NHP sequence described] shown in SEQ ID NO:1.
2. An isolated nucleic acid molecule comprising a nucleotide sequence that:
  - (a) ]encodes the amino acid sequence shown in SEQ ID NO:2[; and
  - (b) hybridizes under stringent conditions to the nucleotide sequence of SEQ ID NO: 1 or the complement thereof].
3. An isolated nucleic acid molecule comprising a nucleotide sequence that encodes the amino acid sequence shown in SEQ ID NO:4.
4. An isolated nucleic acid molecule comprising a nucleotide sequence that encodes the amino acid sequence shown in SEQ ID NO:6.
5. An isolated nucleic acid molecule comprising a nucleotide sequence that encodes the amino acid sequence shown in SEQ ID NO:8.
6. An isolated nucleic acid molecule comprising a nucleotide sequence that encodes the amino acid sequence shown in SEQ ID NO:10.
- 7.(New) An expression vector comprising a nucleic acid sequence of Claim 2.
- 8.(New) A cell comprising the expression vector of Claim 7.

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# NiceProt View of TrEMBL: Q9UGD3

SEP 16 2002

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[\[Sequence\]](#) [\[Tools\]](#)

## General information about the entry

Entry name **Q9UGD3**Primary accession number **Q9UGD3**Secondary accession numbers **None**Entered in TrEMBL in **Release 13, May 2000**Sequence was last modified in **Release 17, June 2001**Annotations were last modified in **Release 22, October 2002**

## Name and origin of the protein

Protein name **DJ842G6.2 [Fragment]**Synonym **Novel protein imilar to SEL1L (Sel-1 (Suppressor of lin-12, C.elegans)-like)**Gene name **DJ842G6.2**From **Homo sapiens (Human) [TaxID: 9606]**Taxonomy **Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.**

## References

[1] SEQUENCE FROM NUCLEIC ACID.

Barlow K.;

Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.

## Comments

None

## Cross-references

EMBL **AL109657; CAB65792.2; -. [[EMBL](#) / [GenBank](#) / [DDBJ](#)] [[CoDingSequence](#)]**Genew **HGNC:15897; C20orf50.**Ensembl **Q9UGD3; Homo sapiens. [[Entry](#) / [Contig view](#)]**ProtoMap **Q9UGD3.**PRESAGE **Q9UGD3.**ModBase **Q9UGD3.**SWISS-2DPAGE **GET REGION ON 2D PAGE.**

## Keywords

None

## Features

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Key From To Length Description  
NON\_TER 1 1



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# Sequence information

Length: **505 AA** [This is the length of the partial sequence]  
Molecular weight: **57003 Da** [This is the MW of the partial sequence]

CRC64: **536D4361FA826E35** [This is a checksum on the sequence]

10	20	30	40	50	60
ALGFLSSYGI	GMEYDQAKAL	IYYTFGSAGG	NMMSQMILGY	RYLSGINVLQ	NCEVALSYK
70	80	90	100	110	120
KVADYIADTF	EKSEGVPEK	VRLTERPENL	SSNSEILDWD	IYQYYKFLAE	RGDVQIQVSL
130	140	150	160	170	180
GQLHLIGRKG	LDQDYKALH	YFLKAAKAGS	ANAMAFIGKM	YLEGNAAVPQ	NNATAFKYFS
190	200	210	220	230	240
MAASKGNAIG	LHGLGLLYFH	GKGVPLNYAE	ALKYFQKAAE	KGWPDAQFQL	GFMYYSGSGI
250	260	270	280	290	300
WKDYKLAFKY	FYLASQSGQP	LAIYYLAKMY	ATGTGVVRSC	RTAVELYKGV	CELGHWAEEK
310	320	330	340	350	360
LTAYFAYKDG	DIDSSLVQYA	LLAEMGYEVA	QSNSAFILS	KKANILEKEK	MYPMALLLWN
370	380	390	400	410	420
RAAIQGNFA	RVKIGDYHY	GYGTTKDYQT	AATHYSIAAN	KYHNAQAMFN	LAYMYEHGLG
430	440	450	460	470	480
ITKDIHLARR	LYDMAAQTS	DAHIPVLFV	MKLETTLLR	DILFFNFTTR	WNWLKLDNTI
490	500				
GPHWDLFVIG	LIVPGLILL	RNHHG			

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Q9UGD3 in [FASTA format](#)

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Direct BLAST submission at  
[EMBnet-CH/SIB \(Switzerland\)](#)



Direct BLAST submission at [NCBI \(Bethesda, USA\)](#)

Sequence analysis tools: [ProtParam](#), [ProtScale](#),

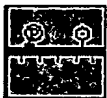


[ScanProsite](#), [MotifScan](#)

Tools



[Compute pI/Mw](#), [PeptideMass](#), [PeptideCutter](#),  
[Dotlet \(Java\)](#)



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FASTA searches a protein or DNA sequence data bank  
version 3.3t05 March 30, 2000

Please cite:

W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

/tmp/fastaCAA\_Xa40t: 689 aa  
>FIRST\_SEQUENCE  
vs /tmp/fastaDAAaYa40t library  
searching /tmp/fastaDAAaYa40t library

505 residues in 1 sequences

FASTA (3.34 January 2000) function [optimized, BL50 matrix (15:-5)] ktup: 2  
join: 38, opt: 26, gap-pen: -12/ -2, width: 16  
Scan time: 0.033

The best scores are: opt  
tr|Q9UGD3 DJ842G6.2 (Novel protein imilar to SEL1 ( 505) 3344

>>tr|Q9UGD3 DJ842G6.2 (Novel protein imilar to SEL1L (Se (505 aa)  
initn: 3342 initl: 3071 opt: 3344  
Smith-Waterman score: 3344; 99.802% identity in 506 aa overlap (184-689:1-505)

	160	170	180	190	200	210
FIRST_	LFGNFGVQ	NITAAIQ	LYESLAKE	GSCKAQNA	LGLSSYG	IGMEYDQA
	KALIIYYTFGSAGG					
	.....					
tr Q9U				ALGFLSS	YGIGMEY	DQA
				KALIIYYTFGSAGG		
				10	20	30

	220	230	240	250	260	270
FIRST_	NMMSQMIL	GYRYLSG	INVLQNC	EVALSYK	KKVADYI	ADTFEKSE
	GVPVEKVRLTERPENL					
	.....					
tr Q9U	NMMSQMIL	GYRYLSG	INVLQNC	EVALSYK	KKVADYI	ADTFEKSE
	GVPVEKVRLTERPENL					
	40	50	60	70	80	90

	280	290	300	310	320	330
FIRST_	SSNSEILD	WDIYQY	KFLAERG	DVQIQV	SLGQLHL	IGRKGLD
	QDYKALHYFLKAAKAGS					
	.....					
tr Q9U	SSNSEILD	WDIYQY	KFLAERG	DVQIQV	SLGQLHL	IGRKGLD
	QDYKALHYFLKAAKAGS					
	100	110	120	130	140	150

	340	350	360	370	380	390
FIRST_	ANAMAFIG	KMYLEG	NAAVPQN	NATAFKY	FSMASKG	NAIGLHGL
	LGLLYFHGKGVPLNYAE					
	.....					
tr Q9U	ANAMAFIG	KMYLEG	NAAVPQN	NATAFKY	FSMASKG	NAIGLHGL
	LGLLYFHGKGVPLNYAE					
	160	170	180	190	200	210

	400	410	420	430	440	450
FIRST_	ALKYFQKA	AEKGWPD	AQFQLGF	MYYSGSG	IWKDYKL	AFKYFYLA
	SQSGQPLAIYYLAKMY					
	.....					
tr Q9U	ALKYFQKA	AEKGWPD	AQFQLGF	MYYSGSG	IWKDYKL	AFKYFYLA
	SQSGQPLAIYYLAKMY					
	220	230	240	250	260	270

	460	470	480	490	500	510
FIRST_	ATGTGVVR	SCRTA	VELYKGV	CELGHWA	EKFLTAY	FAYKDG
	DIDSSLVQYALLAEMGYEVA					
	.....					
tr Q9U	ATGTGVVR	SCRTA	VELYKGV	CELGHWA	EKFLTAY	FAYKDG
	DIDSSLVQYALLAEMGYEVA					
	280	290	300	310	320	330

	520	530	540	550	560	570
FIRST_	QNSAFILE	SKKANILE	KEKMPMA	LLLNRAAI	QGNAFAR	VKIGDYHY
	GYGYGTTKDDYQT					

```

.....
tr|Q9U QSNSAFILSKKANILEKEKMYPMALLLWNRAAIQGNAFARVKIGDYHYGYGTTKDYQT
      340      350      360      370      380      390

      580      590      600      610      620      630
FIRST_ AATHYSIAANKYHNAQAMFNLAYMYEHGLGITKDIHLARRLYDMAAQTSPDAHIPVLFVAV
      .....
tr|Q9U AATHYSIAANKYHNAQAMFNLAYMYEHGLGITKDIHLARRLYDMAAQTSPDAHIPVLFVAV
      400      410      420      430      440      450

      640      650      660      670      680
FIRST_ MKLETTHLLRDILFFNQFTTRWNWLKLDNTIGPHWDLFVIGLIVPGLILLLRNHHG
      .....
tr|Q9U MKLETTHLLRDILFFN-FTTRWNWLKLDNTIGPHWDLFVIGLIVPGLILLLRNHHG
      460      470      480      490      500

```

689 residues in 1 query sequences  
 505 residues in 1 library sequences  
 Scomplib [version 3.3t05 March 30, 2000]  
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 Scan time: 0.033 Display time: 0.434

Function used was FASTA